

At page 11, replace the third paragraph with the following:

Figure 3. A) (SEQ ID NOS: 11 & 12) Structure and sequence of the protein coding region of the putative human B7RP1 (hB7RP1). Predicted signal sequence of hB7RP1 is underlined at the amino-terminus. Predicted signal peptide cleavage sites are marked by asterisks. Predicted transmembrane sequence is underlined toward the carboxy-terminus. B) (SEQ ID NOS: 13, 14 & 15) Amino acid alignment of the putative mature hB7RP1 protein with the mature murine B7RP1 (mB7RP1) protein.

At page 15, replace the last paragraph with the following:

Figure 12. A) (SEQ ID NOS: 16 & 17) Structure and sequence of the protein coding region of human B7RP1 (hB7RP1). Predicted signal sequence of hB7RP1 is underlined at the amino-terminus. Predicted signal peptide cleavage sites are marked by asterisks. Predicted transmembrane sequence is underlined toward the carboxy-terminus. B) (SEQ ID NOS: 18, 19 & 20) Amino acid alignment of the putative mature hB7RP1 protein with the mature murine B7RP1 (mB7RP1) protein.

At page 16, replace the first paragraph with the following:

Figure 13. A) (SEQ ID NOS: 21 & 22) Structure and sequence of the protein coding region of human CRP1 (hCRP1). Predicted signal sequence of hCRP1 is underlined at the amino-terminus. Predicted signal peptide cleavage sites are marked by asterisks. Predicted transmembrane sequence is underlined toward the carboxy-terminus. B) (SEQ ID NOS: 23 & 24) Amino acid alignment of the hCRP1 protein with the murine CRP1 (mB7RP1) protein.

In the claims:

Please replace Claim 2 with the following:

2. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

- the nucleotide sequence as set forth in Figure 2A (SEQ ID NO: 6) or Figure 3A (SEQ ID NO: 11) or Figure 12A (SEQ ID NO: 16);
- the nucleotide sequence encoding the polypeptide as set forth in Figure 2A (SEQ ID NO: 6) from residues 1-322 or from residues 47-322, or as set forth in Figure 3A (SEQ ID NO: 11) from residues 1-288 or from residues 19-288, 20-288, 21-288, 22-288, 24-288, or 28-288 or as set forth in Figure 12A (SEQ ID NO: 16) from residues 1-302, or from residues 19-302, 20-302, 21-302, 22-302, 24-302 or 28-302;
- a nucleotide sequence encoding a polypeptide that is at least about 70 percent identical to the polypeptide as set forth in Figure 2A (SEQ ID NO: 6) or Figure 3A (SEQ ID NO: 11) or Figure 12A (SEQ ID NO: 6);
- a naturally occurring allelic variant or alternate splice variant of any of (a), (b) or (c);